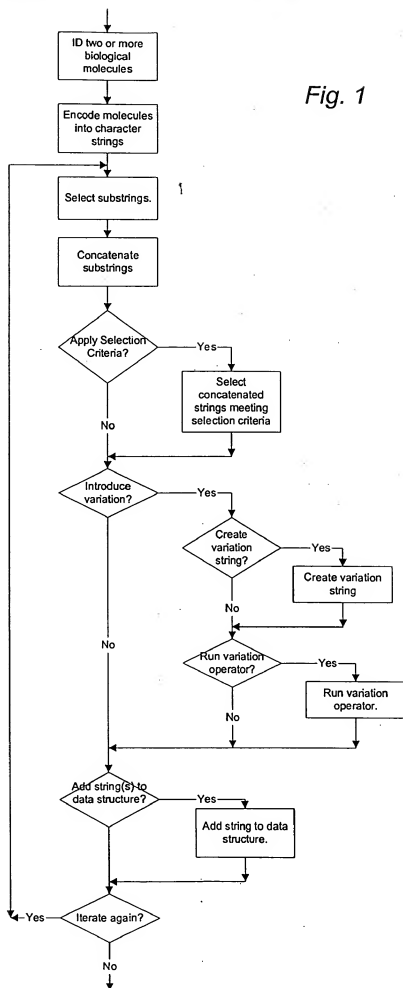


Fig. 1



3271.002US0

Initial strings A, B, and C:

String A: A1 - A2 - A3 - A4 - A5  
String B: B1 - B2 - B3 - B4 - B5  
String C: C1 - C2 - C3 - C4 - C5

↓  
Select substrings

String Pools:

Pool 1: A1, B1, C1  
Pool 2: A2, B2, C2  
Pool 3: A3, B3, C3

↓  
Concatenate  
substrings

New Strings:

String A: A1 - B2 - B3 - C4 - A5  
String B: B1 - C2 - C3 - B4 - B5  
String C: C1 - A2 - A3 - A4 - C5

*Fig. 2*

3271.002W00

Initial sequences



Subsequences aligned  
by similarity



Concatenated  
subsequences



*Fig. 3*

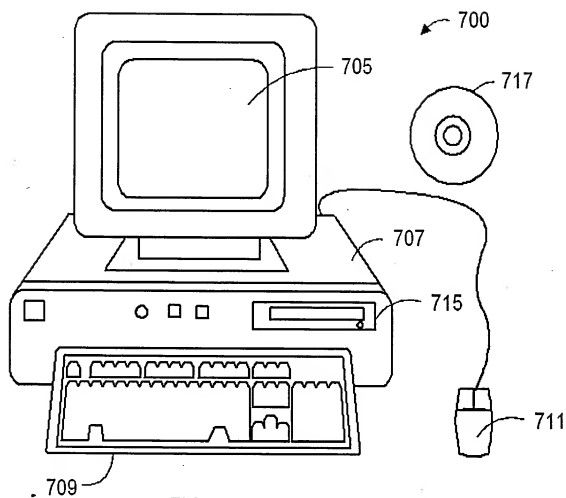


FIG. \_\_\_\_

**Fig. 4**

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Fig. 5

## FAMILY GAGGS MODEL # 1.

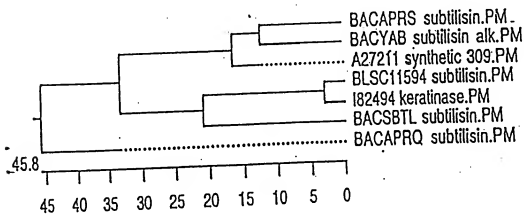
SUBTILISIN BACKGROUND INFORMATION:

7 PARENTS, SERINE PROTEASES, DIVERSE

TYPE OF ALIGNMENT/SIMILARITY DATA PRESENTED:  
AMINOACID SEQUENCES, LEADER PEPTIDE EXCLUDED.

Percent Similarity

	1	2	3	4	5	6	7		
1	████	62.1	81.4	57.6	81.8	56.1	59.1	1	A27211 synthetic 309.PM
2	50.5	████	61.0	54.9	59.5	58.2	60.8	2	BACAPRQ subtilisin.PM
3	21.0	52.0	████	54.6	78.4	50.6	53.2	3	BACAPRS subtilisin.PM
4	54.4	63.3	62.3	████	52.0	64.6	67.9	4	BACS8TL subtilisin.PM
5	20.5	54.9	25.1	65.6	████	53.9	56.5	5	BACYAB subtilisin alk.PM
6	58.6	56.6	72.2	44.2	63.4	████	94.9	6	BLSC11594 subtilisin.PM
7	52.5	51.4	66.0	38.5	57.8	4.9	████	7	I82494 keratinase.PM
	1	2	3	4	5	6	7		



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Fig. 6

FAMILY GAGGS: SUBTILISIN MODEL: PAIRWISE DOT-PLOT ALIGNMENTS TO FIND HOMOLOGY AREAS

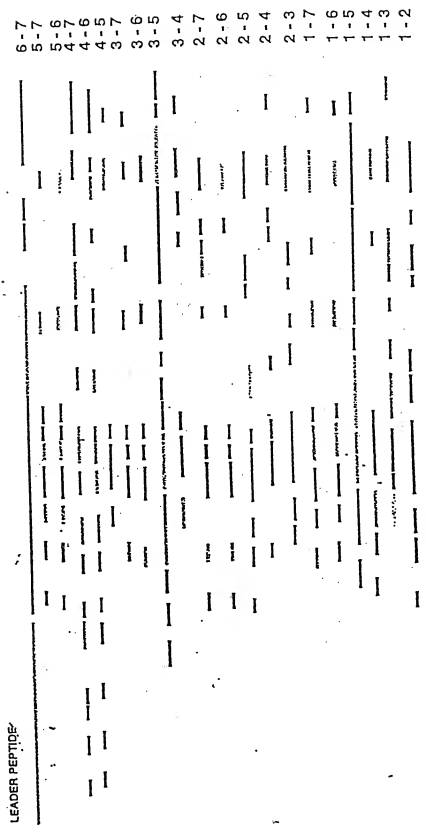


Fig. 7

## GAGGS - SUBTILISIN MODEL (7 PARENTS) SELECTING PAIRWISE Crossover POINTS

## LEADER PEPTIDE

